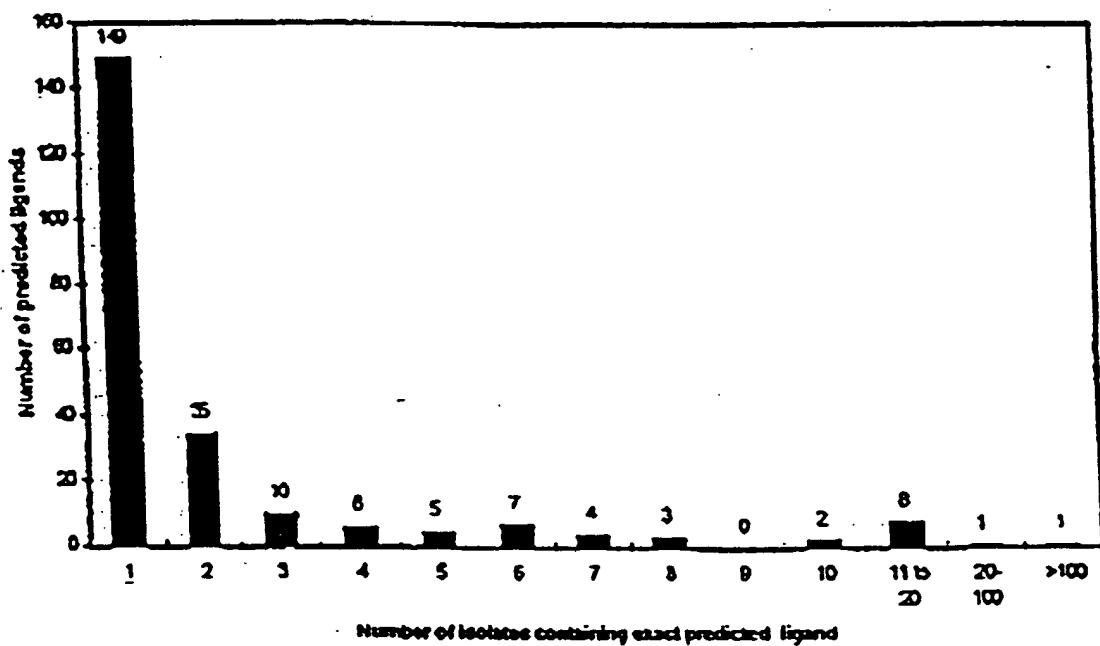


FIG. 1

a)



b)

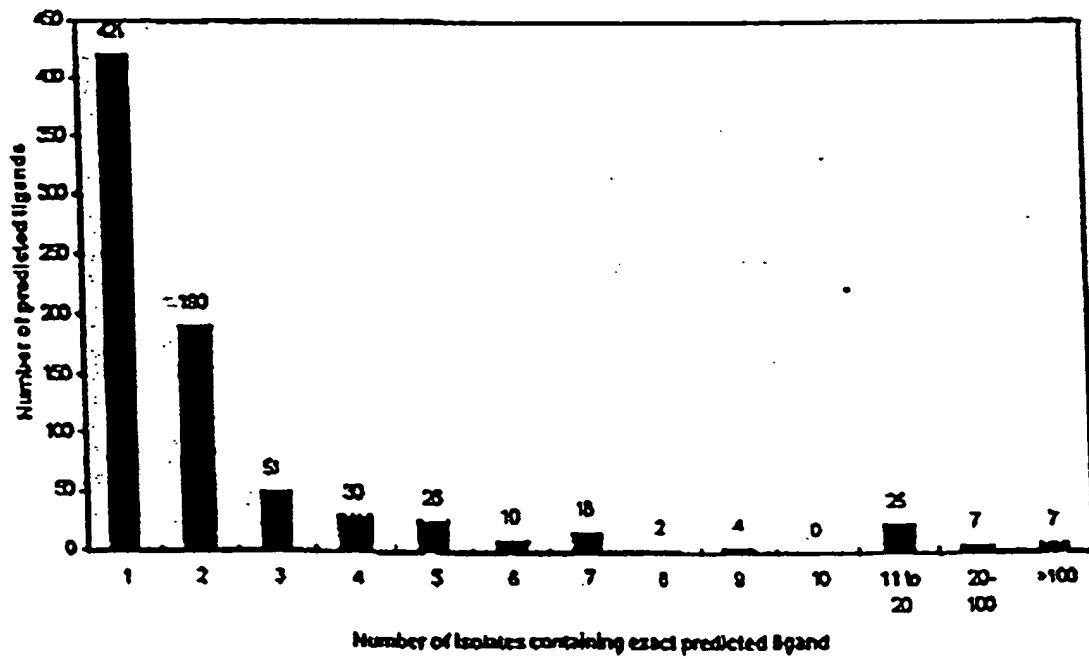


FIG. 2

Sequence	A2 EBP	B27 EBP	A2 Fold Increase (less than 1.3 not reported)	B27 Fold Increase (less than 1.3 not reported)	Protein Isolates with Exact AA	Number of Approximate Position in LAI sequence	Clade					Other SEQ ID NO.
							A	B	C	D	E	
KLTPLCVTLN	55.68%	0.00%	1.33		Env	159	gp120 - 120	X	X	X	X	1
AEWDRVHPV	66.42%	0.00%	1.35		Gag	36	gag - 215	X	X	X	X	2
SLFNTVATL	62.00%	0.00%			Gag	18	gag - 100	X	X	X	X	3
ELHPDKWTV	57.03%	0.00%			RT	17	RT - 354	X	X	X	X	4
GMDDPEREVL	72.52%	0.00%	2.7		Nef	17	nef - 170	X	X	X	X	5
GMDDPEKEVL	87.51%	0.01%			Nef	16	nef - 170	X	X	X	X	6
HLWRWGTMLL	76.69%	0.00%	1.33		Env	10	gp120 - 30	X	X	X	X	7
LLLTRDGGVN	55.68%	0.00%			Env	>10	gp120 - 452	X	X	X	X	8
HLWKWSTMLL	90.92%	0.00%	1.63		Env	>10	gp120 - 20	X	X	X	X	9
ILKEPVHGV	97.47%	0.00%	1.54		RT	>10	RT - 480	X	X	X	X	10
KRWLGLNK	0.00%	14.22%	3.61		Gag	79	gag - 263	X	X	X	X	11
CRKQDIN	0.00%	99.08%			Env	183	gp120 - 420	X	X	X	X	12
CRKQDAMW	0.00%	99.52%	1.74		Env	150	gp120 - 420	X	X	X	X	13
VSFEPPIHF	0.20%	55.61%	1.45		Env	109	gp120 - 213	X	X	X	X	14
RCSSNTGL	0.01%	62.11%			Env	101	gp120 - 446	X	X	X	X	15
VSFEPPIHY	0.00%	98.22%			Env	101	gp120 - 213	X	X	X	X	16
CRKQVNM	0.00%	91.33%			Env	75	gp120 - 420	X	X	X	X	17
IRSENTNN	0.00%	82.77%			Env	42	gp120 - 273	X	X	X	X	18
IRFAMV	0.05%	89.06%			Env	19	gp41 - 175	X	X	X	X	19
ISFDPIHY	0.01%	67.49%			Env	15	gp120 - 213	X	X	X	X	20
YRTGDIIG	0.00%	56.14%			Env	15	gp120 - 330	X	X	X	X	21
IRGPQQTFY	0.07%	73.36%			Env	13		X	X	X	X	22
GCSGKIC	0.00%	61.09%			Env	12	gp41 - 90	X	X	X	X	23
RRRAPQDS	0.00%	67.49%			Tat	12		X	X	X	X	24
IRSENTDN	0.00%	59.28%			Env	11	gp120 - 273	X	X	X	X	25
CRKQFIN	0.00%	76.92%	1.53		Env	<10	gp120 - 420	X	X	X	X	26
KRISIGGR	0.00%	56.93%	1.78		Env	<10	gp120 - 320	X	X	X	X	27
GCQQDEQL	0.10%	78.95%			Env	<10	gp41 - 270	X	X	X	X	28
GRRGWELKY	0.01%	59.80%	3.27		Env	<10	gp41 - 270	X	X	X	X	29

FIG. 3

Project Outline

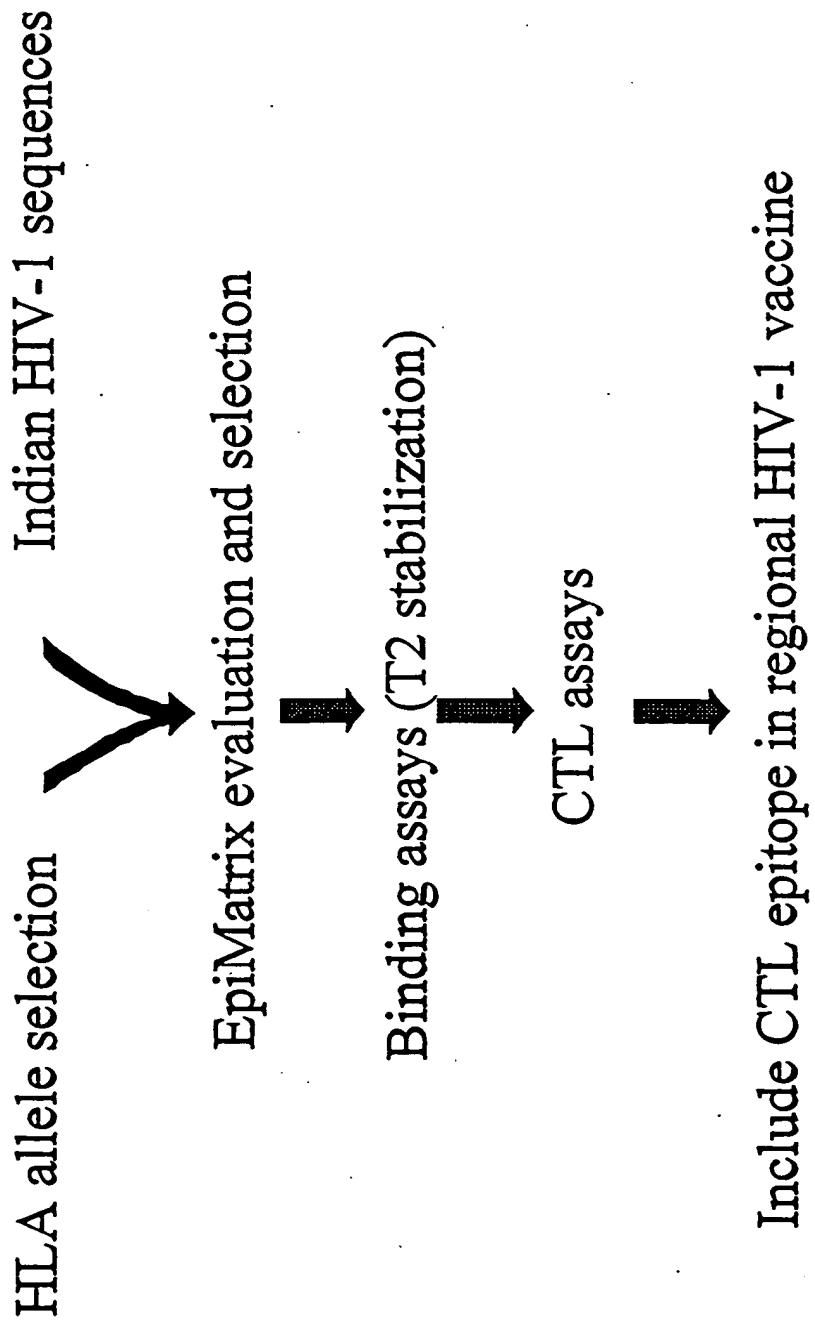
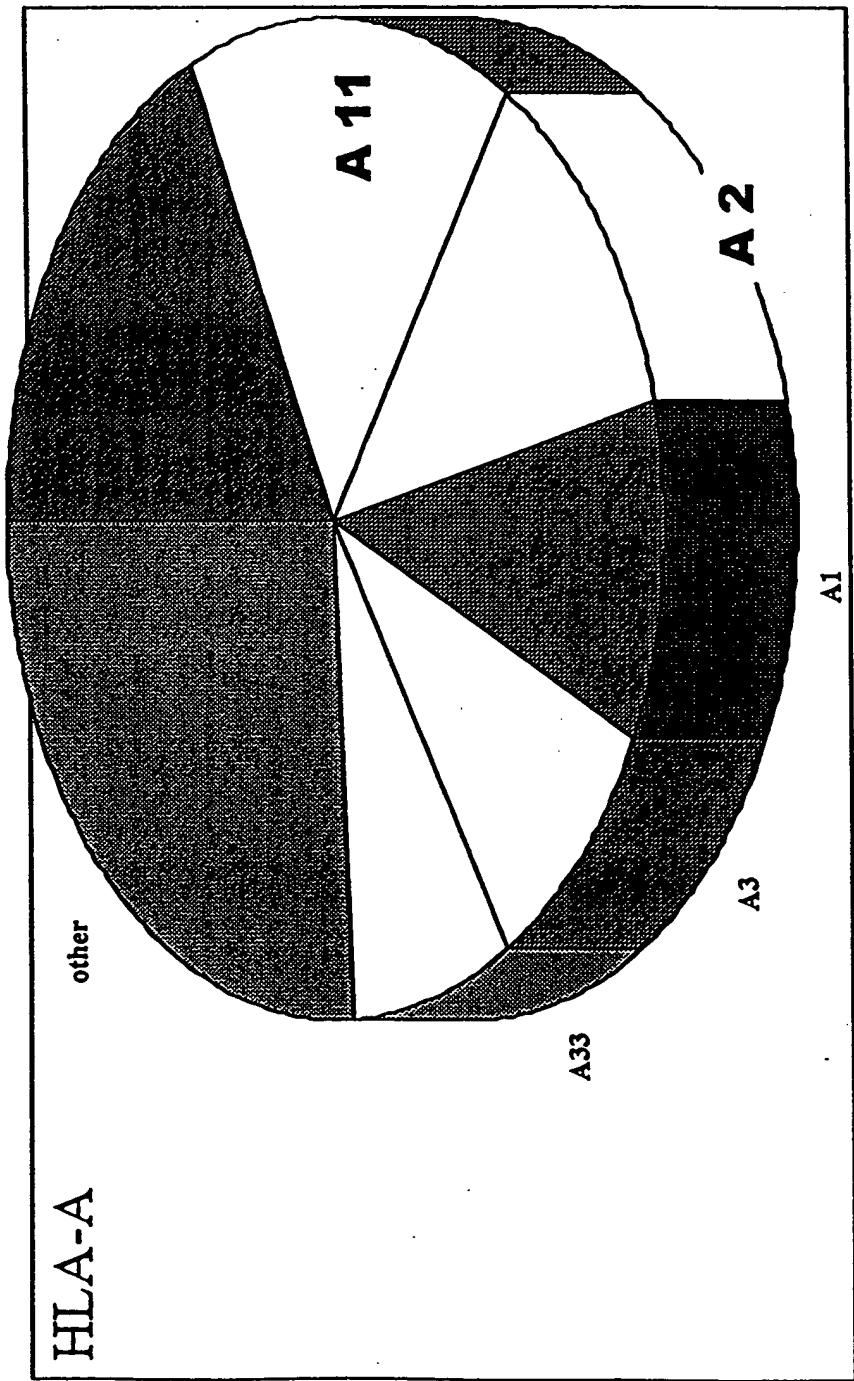
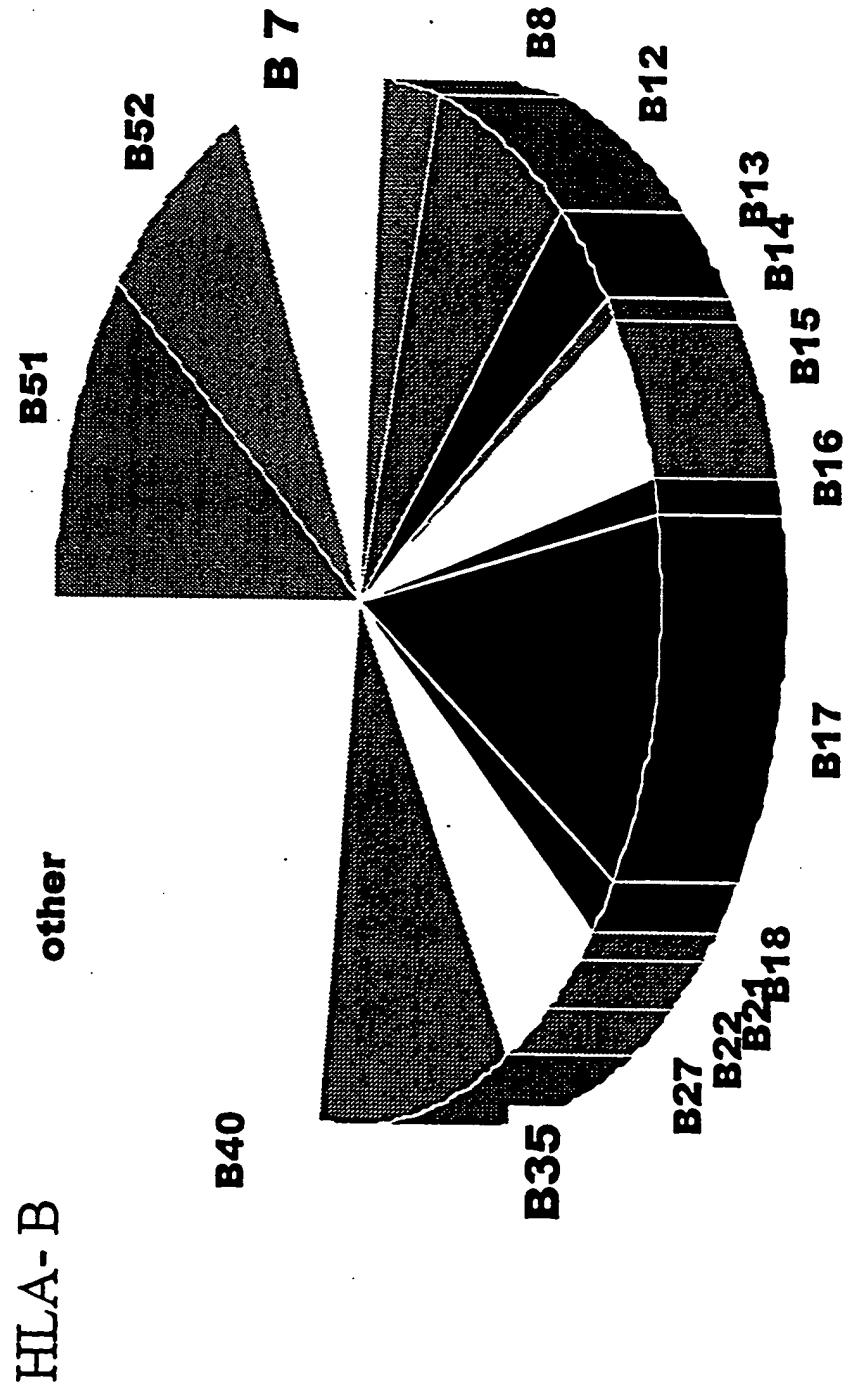


FIG. 4
Methods: HLA allele selection



HLA-A2 and -A11, -B7 and -B35 were selected for this pilot project due to their prevalence of the HLA alleles in the Indian population....

FIG. 5
Methods: HLA allele selection



... and availability of cell lines for *in vitro* study.

FIG. 6
EpiMatrix Predictions and Binding Results: B 7
6 out of 7, and control peptide

B7							
Peptide #	Peptide	seq. Used	gene	strain	start-stop	% conserved	CTL predicted EBP avg MFI (200ug/ml) avg fold incr. (20ug/ml)
1	RPNNNTRKSI	RPNNNTRKSI	ENV	DID757	183-192	75	Y 8% 335.6 2.4
3	NPYNTPIAL	NPYNTPIAL	POL	SoInd5	61-70	60	20% 281.9 2.0
4	RAIEQQHLL	RAIEQQHLL	ENV	DID747	481-490	60	17% 181.5 1.3
5	TCKSNITGLL	TCKSNITGLL	ENV	DID760	375-384	58	18% 160.5 1.2
	KPVYSTQLL	KPVYSTQLL	ENV	DID747	182-191	71	46% 248.6 1.8
	KPCVYKLTPLC	KPCVYKLTPLC	ENV	DID747	61-60	100	27% 373.8 2.7
	GPKVKAQWPL	GPKVKAQWPL	POL	SoInd4	25-34	100	27% 314.7 2.3
	YPGIKVRAQL	YPGIKVRAQL	POL	SoInd4	278-287	100	26% 378.4 2.7

FIG. 7
EpiMatrix Predictions and Binding Results: B 35
7 out of 7 ... and control peptide

B37							
Pepptide #	Peptide	seq. Used	gene	strain	start-stop	% conserved	predicted CTL
2	TVLDVGDAYF	TVLDVGDAYF	POL	Solind4	114-123	100	Y
6	EPPFLWMGY	EPPFLWMGY	POL	Solind4	231-239	100	9%
7	VPVKLKGMD	VPVKLKGMD	POL	Solind4	15-24	100	9%
8	CPKVTFDPI	CPKVTFDPI	ENV	DID780	144-153	53	7%
	KPVNSTQLL	KPVNSTQLL	ENV	DID747	182-191	71	9%
	KPCVKLTPL	KPCVKLTPL	ENV	DID747	51-60	100	11%
	GPKVKQWPL	GPKVKQWPL	POL	Solind4	25-34	100	11%
	YGGIKVRL	YGGIKVRL	POL	Solind4	278-287	100	7%

avg MFI (200ug/ml)

47.9

47.9

48.7

48.7

53.3

53.3

35.0

35.0

40.5

40.5

52.1

52.1

41.2

41.2

40.7

40.7

1.6

1.6

1.7

1.7

1.2

1.2

1.4

1.4

1.7

1.7

1.4

1.4

1.3

1.3

204020 4255500T

FIG. 8
EpiMatrix Predictions and Binding Results: A 2
3 out of 7 ... and control peptide

A2									
peptide #	peptide	seq. Used	gene	strain	start-stop	% conserved	CTL	predicted EBF	avg MFI (200ug/ml)
13	ILKEPVHGV	ILKEPVHGV	POL	SoInd4	316-325	80	Y	88%	1604.2
14	QLPEKDWSITV	QLPEKDWSITV	POL	SoInd4	252-261	100		87%	1368.1
15	NLWTVYYGV	NLWTVYYGV	GrD1024	ENV	32-41	67		84%	1716.9
16	QMHEDVISLW	QMHEDVISLW	ENV	DID747	37-46	91		78%	1413.1
17	KIEELREHLL	KIEELREHLL	POL	SoInd5	208-217	60		79%	889.9
18	DMVNQMHEDV	DMVNQMHEDV	ENV	DID747	33-42	64		77%	731.1
19	GLKKKKSVTV	GLKKKKSVTV	POL	SoInd4	109-115	100		76%	1088.4
20	ELHPDKWTVQ	ELHPDKWTVQ	POL	SoInd4	240-249	80		72%	1046.1

FIG. 9
EpiMatrix Predictions and Binding Results: A 11
4 out of 7 ... and control peptide

A11		peptide #	peptide	seq. Used	gene	strain	start-stop	% conserved	CTL predicted	EPR	avg MFI (200ug/ml)	avg fold incr. (20ug/ml)
21		IYQEPFKNLK	IYQEPFKNLK	POL	Solind4	348-357	100	Y	7%	677.5		3.1
22		VTFDPIHY	VTFDPIHY	ENV	DI760	147-156	53		22%	180.0		0.9
23		TVQCTHGIK	TVQCTHGIK	ENV	DI747	174-183	59		44%	733.4		3.3
24		NTPIFALKKK	NTPIFALKKK	POL	Solind5	64-73	60		44%	187.8		0.9
25		LVDFRELNK	LVDFRELNK	POL	Solind4	81-90	100		47%	755.2		3.4
26		PGMDGPKVK	PGMDGPKVQ	POL	Solind4	21-30	100		52%	183.8		0.7
27		GIPHAGLKK	GIPHAGLKK	POL	Solind4	100-109	100		62%	309.6		1.4
28		FTTPDKKKHQK	FTTPDKKKHQK	POL	Solind4	221-330	100		63%	920.6		4.1

FIG. 10
Methods: T2 Binding Assay

Allele matched peptides stabilize MHC molecules on the surface of TAP deficient cells. The stabilized MHC-peptide complex is detected using Ab to the MHC and fluorescence labeled secondary Ab.

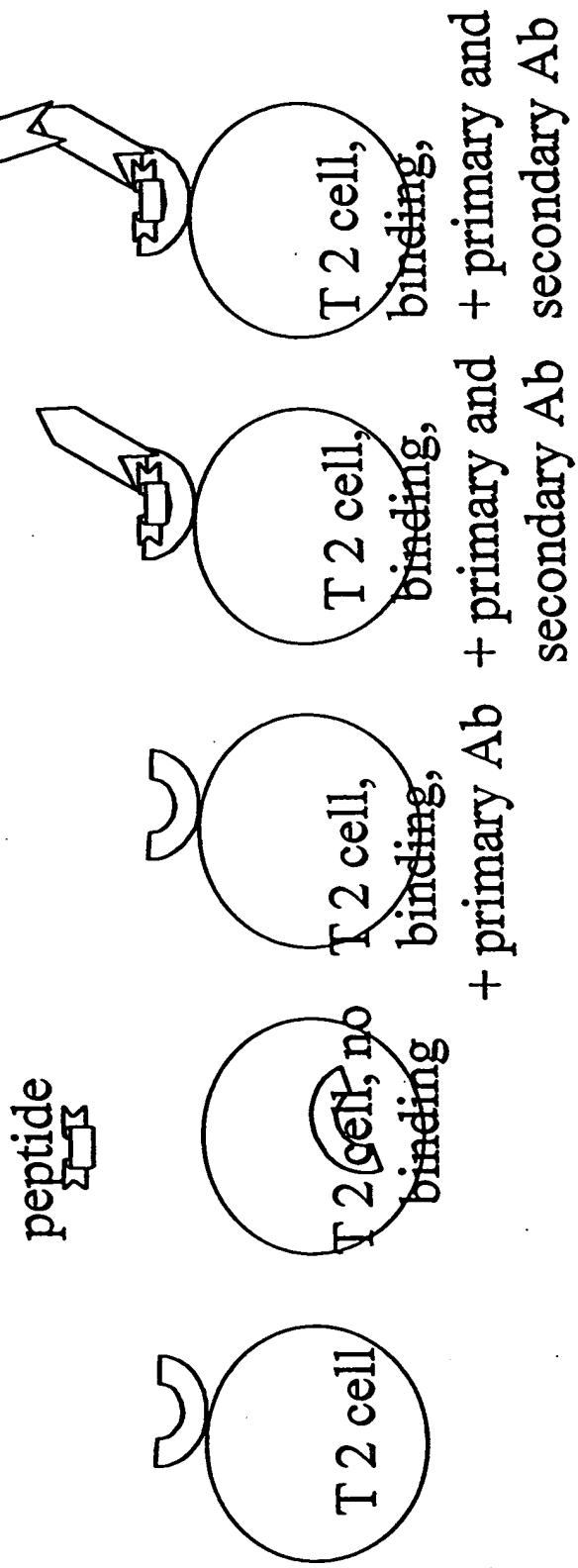
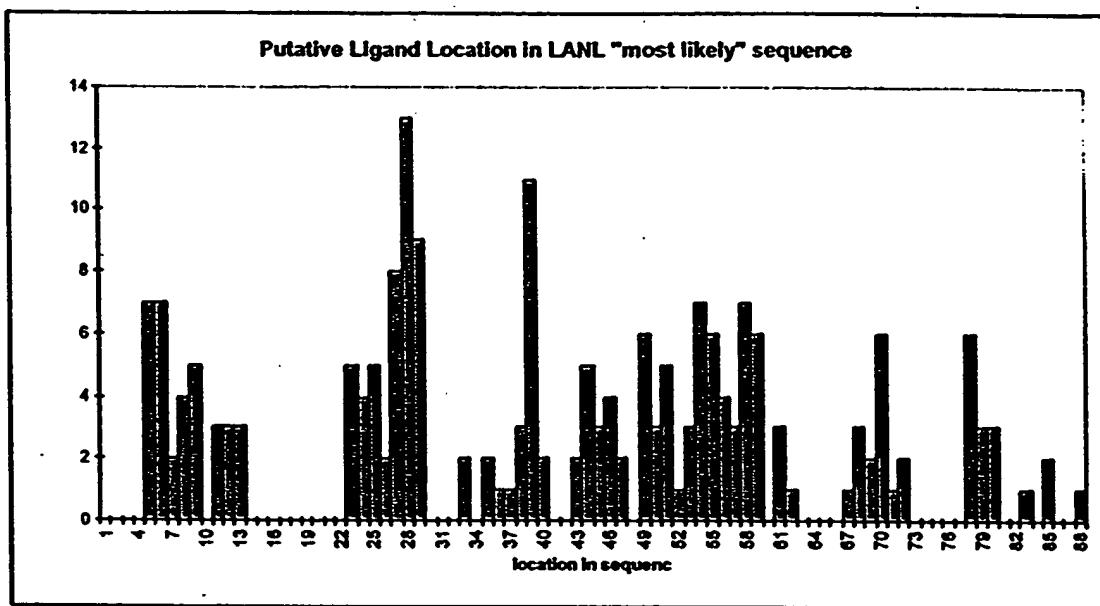


FIG. 11

Clustering of putative MHC ligands in *env*



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